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# Genome Sequence of *Psychrobacter cibarius* Strain W1

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**Here, we report the draft genome sequence of *Psychrobacter cibarius* strain W1, which was isolated at a slaughterhouse in Denmark. The 3.63-Mb genome sequence was assembled into 241 contigs.**

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*Psychrobacter cibarius* belongs to the family *Moraxellaceae* within the class of gammaproteobacteria (1). It is a Gram-negative, nonmotile, rod-shaped or coccoid, psychrophilic, and halotolerant bacterium (2). *P. cibarius* was originally isolated from fermented seafood (2). However, other species within the genus *Psychrobacter* have been identified from diverse environments (1, 3–7). Here, we present the draft assembly of *P. cibarius* strain W1, isolated from a slaughterhouse in Denmark (8). Sequencing libraries were prepared using the Nextera XT kit (Illumina, USA), according to the manufacturer's recommendations, followed by flow cell sequencing with 2 × 250-bp paired-end reads using Illumina MiSeq (Illumina) technology. The reads were cleaned and trimmed with the CLC Genomics Workbench version 7 (CLC bio, Denmark). Both merged and unmerged reads were assembled with SPAdes 3.5.0. The assembled contigs were annotated using the RAST server (9) and RNAmmer server version 1.2 (10) to screen for rRNA genes.

The final genome assembly has an approximate coverage of 117× with a total size of 3,629,624 bp composed of 241 contigs with an average G+C content of 43.7%. Annotation of the genome predicted 3,097 coding sequences (CDSs) (1,437 CDSs have functional predictions), 52 RNA genes, 2 copies of 5S and 16S rRNA genes, and one copy of the 23S rRNA gene. The closest neighbor identified by functional comparison on the RAST server was *P. cryohalolentis* K5 (score, 540) strain. There are 405 subsystems represented in the genome, and metabolic reconstruction revealed genes involved in central carbohydrate metabolism, genes for stress responses including oxidative stress and cold and heat shock. The analysis additionally identified genes responsible for resistance to bacteriocins, resistance to antibiotics and toxic compounds, copper homeostasis, copper tolerance, cobalt-zinc-cadmium resistance, resistance to fluoroquinolones, arsenic resistance, and multidrug resistance efflux pump subsystems. The existence of these genes indicates the adaptation of strain *P. cibarius* W1 to environments with high anthropogenic impact, and future work with the genomes of *Psychrobacter* spp. will give more insights on the evolution and adaptation of these bacteria to diverse environments.

**Nucleotide sequence accession numbers.** The whole-genome shotgun projects for *P. cibarius* strain W1 have been deposited at the European Nucleotide Archive (ENA) under the contig accession numbers CZJV02000001 to CZJV02000241. The versions described in this paper are the first versions.

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